Fig. 1

C

p17M1234

p17M1234(731-1081)
p17M1234(731-1424)
p17M1234(731-2165)

gag

oligonucleotide directed mutagenesis

p17M1234(731-1081)NS

p37M1234

p55BM1234

p17   p24   p15

Fig. 1

A

B

Fig. 2

A

P17   P17R   P17M1234

- + | - + | - + | Rev

— 28S

— 18S

B

P19   P19R

- + | - + | Rev
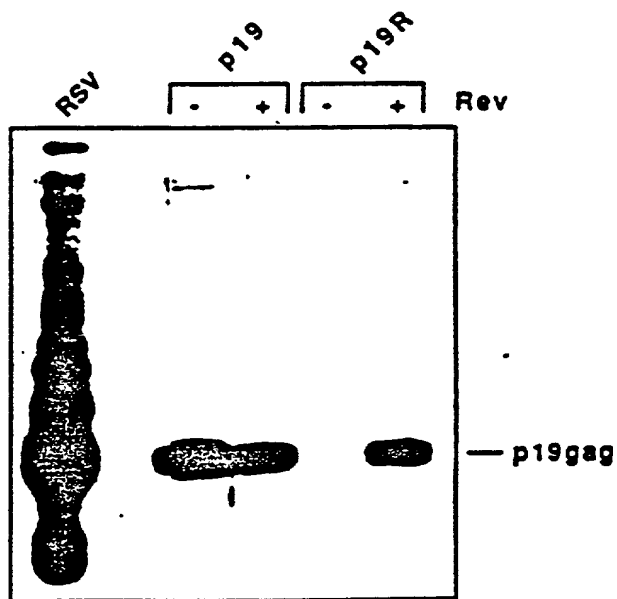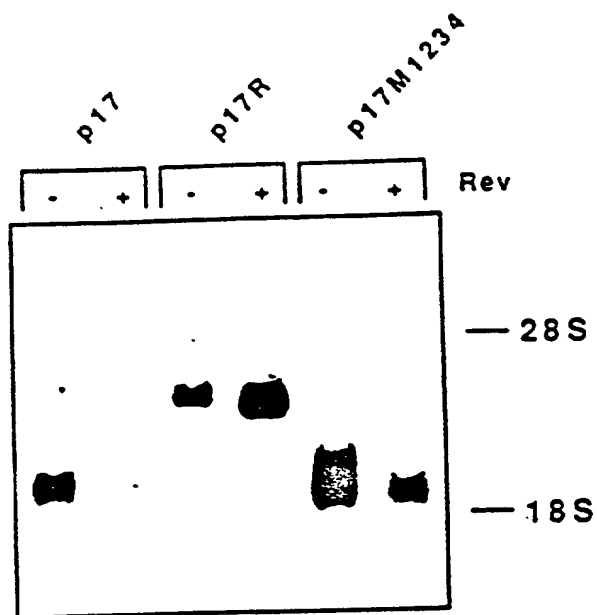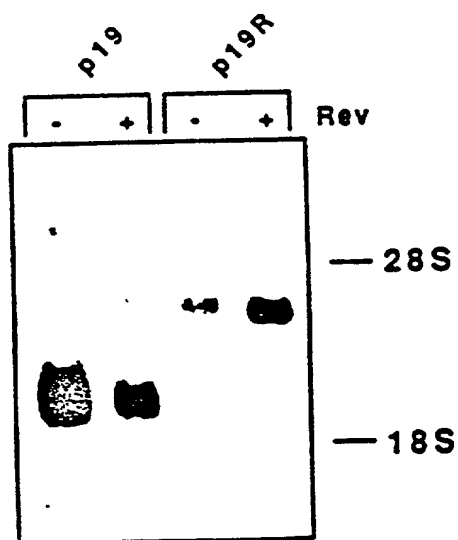
— 28S

— 18S

Fig. 3

```
336
atg ggt gcg aga gcg tca gta tta agc ggg gga gaa tta gat cga tgg gaa aaa att cgg

396                                    M1
tta agg cca ggc gga aag aaa aaa tat aaa tta aaa cat ata gta tgg gca agc agg gag
             G   G   C   G C     G   C   C

456                                                                          -
cta gaa cga ttc gca gtt aat cct ggc ctg tta gaa aca tca gaa ggc tgt aga caa ata

516                                          M2
ctg gga cag cta caa cca tcc ctt cag aca gga tca gaa gaa ctt aga tca tta tat aat
                          G   G   C         C     C   C

576                              M3
aca gta gca acc ctc tat tgt gtg cat caa agg ata gag ata aaa gac acc aag gaa gct
            C   G C     C         C   G

636                                  M4
tta gac aag ata gag gaa gag caa aac aaa agt aag aaa aaa gca cag caa gca gca gct
                          G TCC         G   G   C         G

696
gac aca gga cac agc aat cag gtc agc caa aat tac
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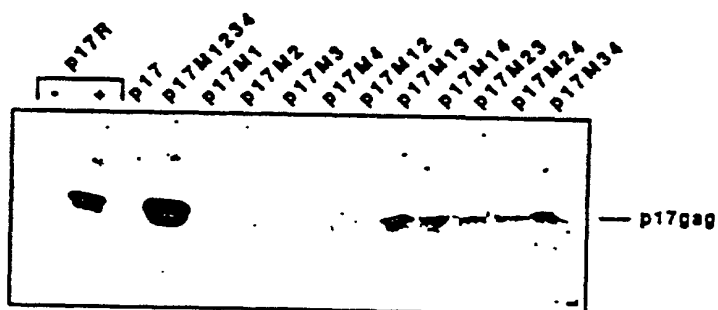
Fig. 4

Fig. 5

Fig. 6
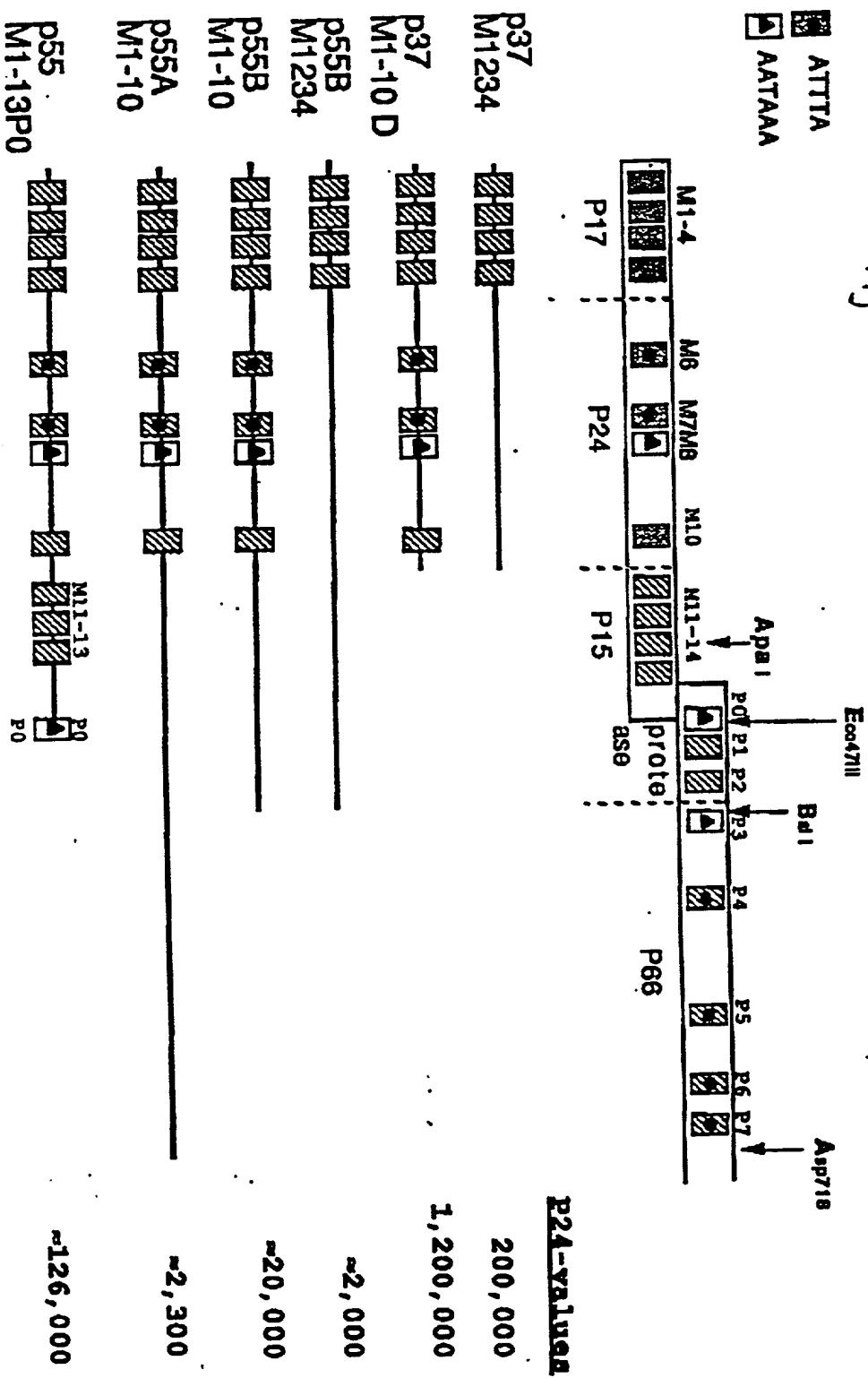
Fig. 7

Fig. 8

Fig. 9

A

Rev

PBS120DSS [− +] P120R270 [− +] P120RD345 [− +] P120PA [− −]

1 2 3 4 5 6 7 8

Fig. 9

B

Rev

| PBS120DSS | | P120R270 | | P120RD345 | | P120PA | |
| - | + | - | + | - | + | - | - |

← gp120
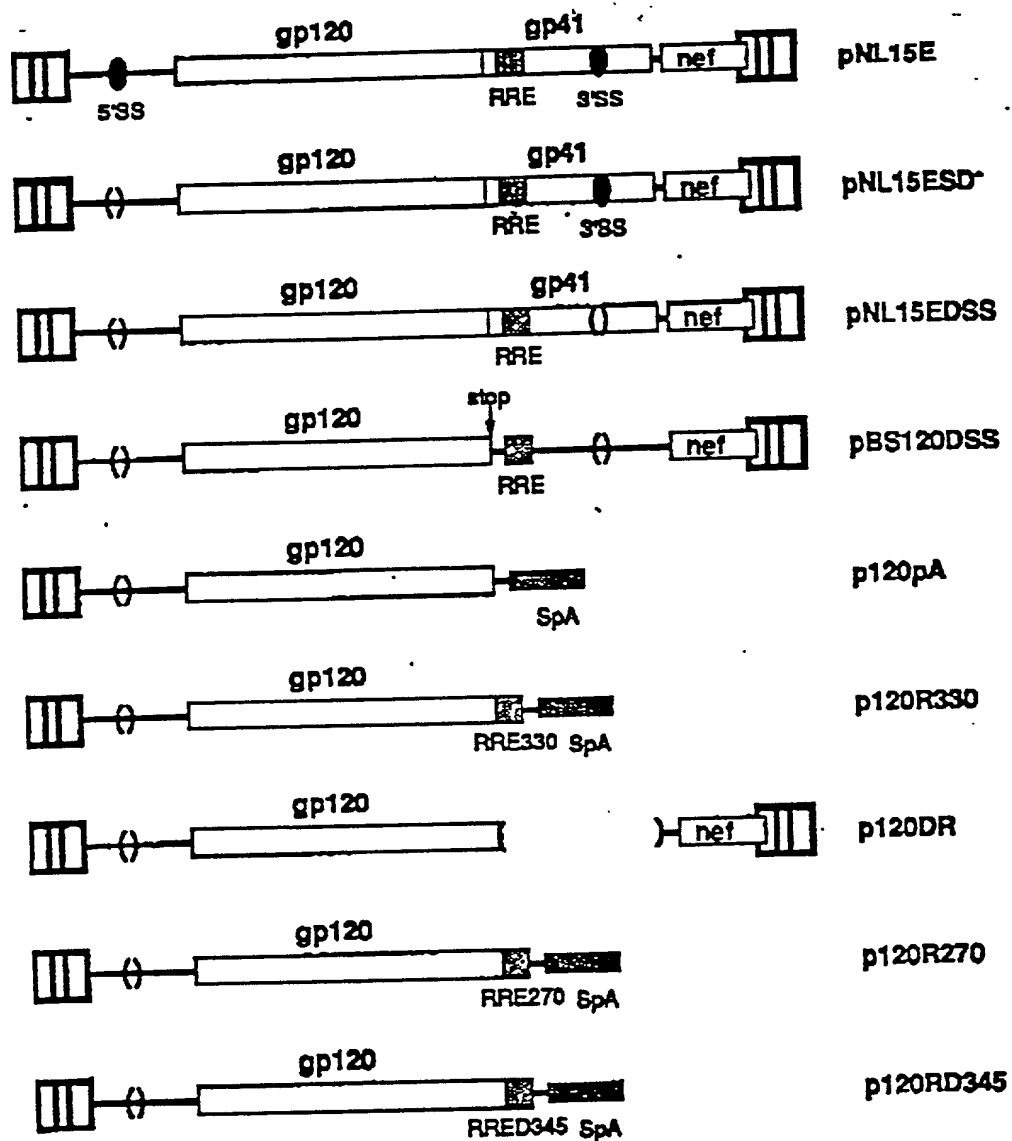
Identification of INS regions within the env mRNA using the p19 vector.

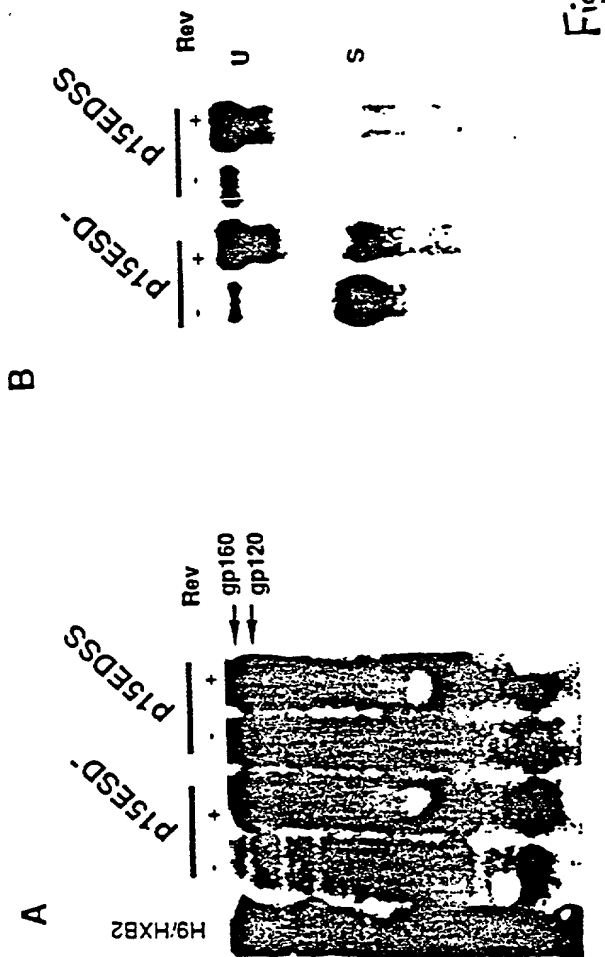| FRAGMENT	SIZE			INS EFFECT
A	276		7684-7959	none
B	234		7684-7884, 7927-7959	none
C	323		7595-7884, 7927-7959	10 X
D	128		7939-8066	none
E	478		7939-8416	10 X
F	362		8200-8561	> 100 X
G	330		7266-7595	3-5X
E	668		5523-6190	10 X

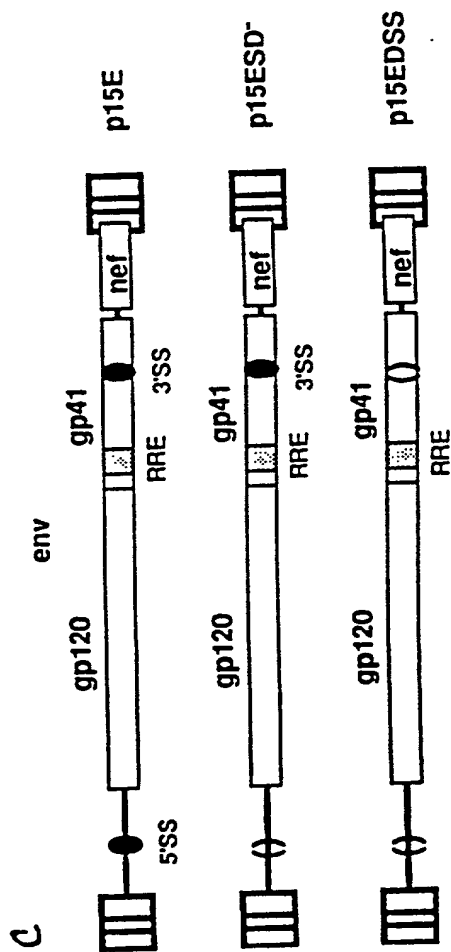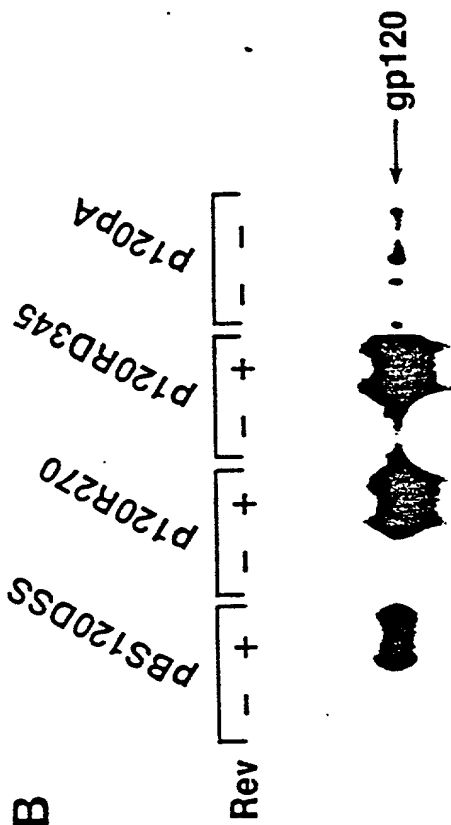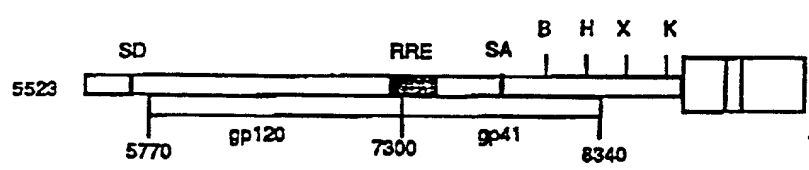Fig. 10

Identification of INS regions within the env mRNA using the p37M1-10D vector.

(fig 5 env, formerly fig D)

p37 M 1-10 D

gag

HIV-1 env

gp120   gp41

	nucleotides:	Decrease in p24
1	(5606-6014)	X 2
2	(6004-6435)	X 7
3	(6435-6878)	X 6
4	(6879-7266)	X 4
5	(7266-7924)	X 34
6	(7925-8807)	NOT DONE
7	(8021-8561)	X 3
1+2	(5606-6435)	X 5
1+2+3	(5606-6878)	X 30
4+5	(6879-7924)	X 22
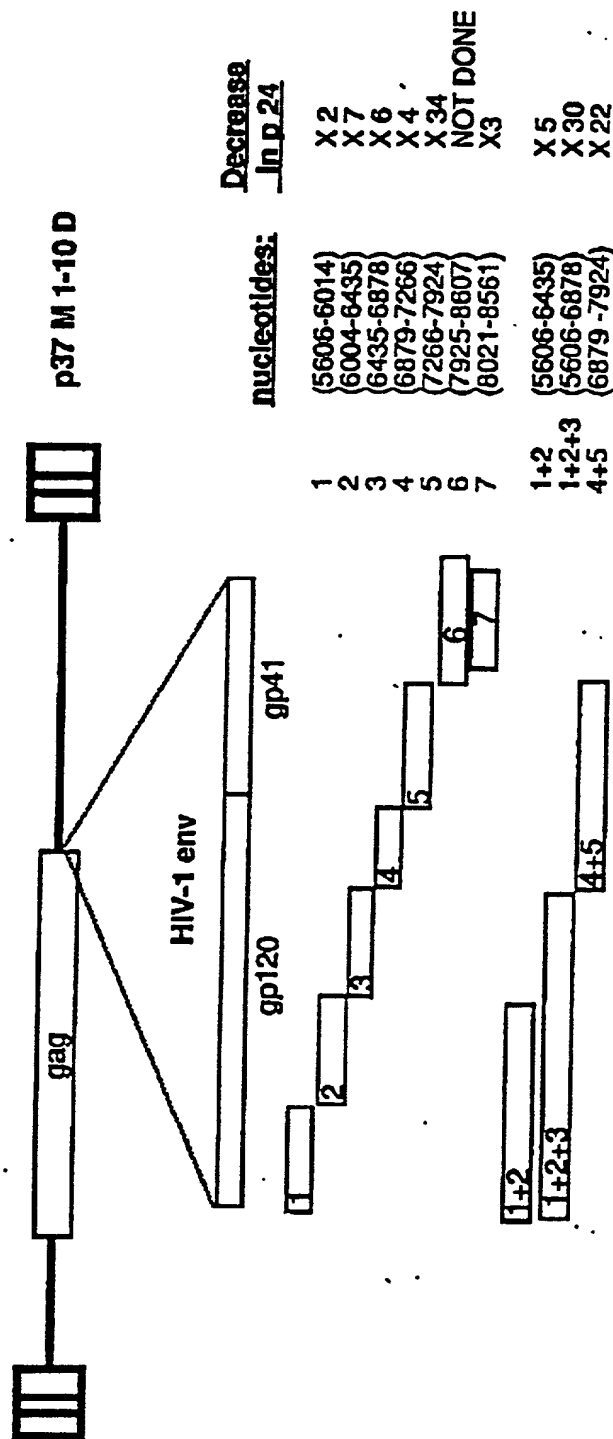
Fig. 11

Elimination of negative effects of CRS
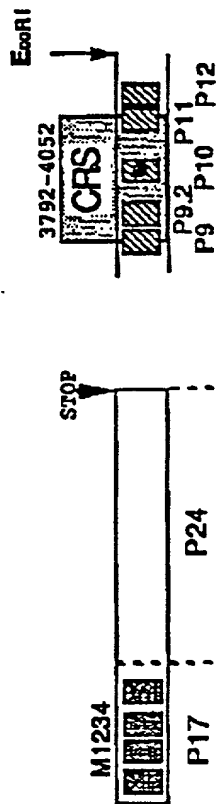
Fig. 12

POINT MUTATIONS ELIMINATING THE NEGATIVE EFFECTS OF CRS IN THE pol REGION

(nucleotides 3700-4194)

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GGTACCAGCACACAAAGGAATTGGAGGAAATGAACAAGTAGATAAATTAGTCAGTGCTGGAATCAGGAAAGTACTATTTT

TAGATGGAATAGATAAGGCCCAAGATGAACATGAGAAATATCACAGTAATTGGAGAGCAATGGCTAGTGATTTTAACCTG

CCACCTGTAGTAGCAAAAGAAATAGTAGCCAGCTGTGATAAATGTCAGCTAAAAGGAGAAGCCATGCATGGACAAGTAGA

CTGTAGTCCAGGAATATGGCAACTAGATTGTACACATTTAGAAGGAAAAGTTATCCTGGTAGCAGTTCATGTGAGCCAGTG
                g  g  c  c  g  cc g  g  g  g  g

GATATATAGAAGCAGAAGTTATTCCAGCAGAAACAGGGCAGGAAACAGCATATTTTCTTTTAAAATTAGCAGGAAGATGG

CCAGTAAAAACAATACATACTGACAATGGCAGCAATTTCACCGGTGCTACGGTTAGGGCCGCCTGTTGGTGGGCGGGAAT
                c  g     c  a     c  t
                c  g     c  a     c

CAAGCAGGAATTTGG
```

Fig. 13

Fig. 14

A

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   1 TGGAAGGGCT AATTTGGTCC CAAAAAAGAC AAGAGATCCT TGATCTGTGG ATCTACCACA CACAAGGCTA

  71 CTTCCCTGAT TGGCAGAACT ACACACCAGG GCCAGGGATC AGATATCCAC TGACCTTTGG ATGGTGCTTC

 141 AAGTTAGTAC CAGTTGAACC AGAGCAAGTA GAAGAGGCCA AATAAGGAGA GAAGAACAGC TTGTTACACC

 211 CTATGAGCCA GCATGGGATG GAGGACCCGG AGGGAGAAGT ATTAGTGTGG AAGTTTGACA GCCTCCTAGC

 281 ATTTCGTCAC ATGGCCCGAG AGCTGCATCC GGAGTACTAC AAAGACTGCT GACATCGAGC TTTCTACAAG

 351 GGACTTTCCG CTGGGGACTT TCCAGGGAGG TGTGGCCTGG GCGGGACTGG GGAGTGGCGA GCCCTCAGAT

 421 GCTACATATA AGCAGCTGCT TTTTGCCTGT ACTGGGTCTC TCTGGTTAGA CCAGATCTGA GCCTGGGAGC
                                      ▶

 491 TCTCTGGCTA ACTAGGGAAC CCACTGCTTA AGCCTCAATA AAGCTTGCCT TGAGTGCTCA AAGTAGTGTG
                                                                              ┤

 561 TGCCCGTCTG TTGTGTGACT CTGGTAACTA GAGATCCCTC AGACCCTTTT AGTCAGTGTG GAAAATCTCT

 631 AGCAGTGGCG CCCGAACAGG GACTTGAAAG CGAAAGTAAA GCCAGAGGAG ATCTCTCGAC GCAGGACTCG
     ─────▶ ─────────────────▶
              BssHII (711)
 701 GCTTGCTGAAGCGCGCGTCGACAGAGAGATGGGTGCGAGAGCGTCAGTATTAAGCGGGGGAGAATTAGATCGATGG
                                       1▶MetGlyAlaArgAlaSerValLeuSerGlyGlyGluLeuAspArgTrp

 777 GAAAAAATTCGGTTAAGGCCAGGGGGAAAGAAGAAGTACAAGCTAAAGCACATCGTATGGGCAAGCAGGGAGCTAG
     17▶GluLysIleArgLeuArgProGlyGlyLysLysLysTyrLysLeuLysHisIleValTrpAlaSerArgGluLeuG

 853 AACGATTCGCAGTTAATCCTGGCCTGTTAGAAACATCAGAAGGCTGTAGACAAATACTGGGACAGCTACAACCATC
     42▶luArgPheAlaValAsnProGlyLeuLeuGluThrSerGluGlyCysArgGlnIleLeuGlyGlnLeuGlnProSe

 929 CCTTCAGACAGGATCAGAGGAGCTTCGATCACTATACAACACAGTAGCAACCCTCTATTGTGTGCACCAGCGGATC
     67▶rLeuGlnThrGlySerGluGluLeuArgSerLeuTyrAsnThrValAlaThrLeuTyrCysValHisGlnArgIle

1005 GAGATCAAGGACACCAAGGAAGCTTTAGACAAGATAGAGGAAGAGCAAAACAAGTCCAAGAAGAAGGCCCAGCAGG
     93▶GluIleLysAspThrLysGluAlaLeuAspLysIleGluGluGluGlnAsnLysSerLysLysLysAlaGlnGlnA

1081 CAGCAGCTGACACAGGACACAGCAATCAGGTCAGCCAAAATTACCCTATAGTGCAGAACATCCAGGGGCAAATGGT
     118▶laAlaAlaAspThrGlyHisSerAsnGlnValSerGlnAsnTyrProIleValGlnAsnIleGlnGlyGlnMetVa
                                                     ▶

1157 ACATCAGGCCATATCACCTAGAACTTTAAATGCATGGGTAAAAGTAGTAGAAGAGAAGGCTTTCAGCCCAGAAGTG
     11▶lHisGlnAlaIleSerProArgThrLeuAsnAlaTrpValLysValValGluGluLysAlaPheSerProGluVal

1233 ATACCCATGTTTTCAGCATTATCAGAAGGAGCCACCCCACAGGACCTGAACACGATGTTGAACACCGTGGGGGGAC
     37▶IleProMetPheSerAlaLeuSerGluGlyAlaThrProGlnAspLeuAsnThrMetLeuAsnThrValGlyGlyH

1309 ATCAAGCAGCCATGCAAATGTTAAAAGAGACCATCAATGAGGAAGCTGCAGAATGGGATAGAGTGCATCCAGTGCA
     62▶isGlnAlaAlaMetGlnMetLeuLysGluThrIleAsnGluGluAlaAlaGluTrpAspArgValHisProValHi

1385 TGCAGGGCCTATTGCACCAGGCCAGATGAGAGAACCAAGGGGAAGTGACATAGCAGGAACTACTAGTACCCTTCAG
     87▶sAlaGlyProIleAlaProGlyGlnMetArgGluProArgGlySerAspIleAlaGlyThrThrSerThrLeuGln

1461 GAACAAATAGGATGGATGACAAATAATCCACCTATCCCAGTAGGAGAGATCTACAAGAGGTGGATAATCCTGGGAT
     113▶GluGlnIleGlyTrpMetThrAsnAsnProProIleProValGlyGluIleTyrLysArgTrpIleIleLeuGlyL

1537 TGAACAAGATCGTGAGGATGTATAGCCCTACCAGCATTCTGGACATAAGACAAGGACCAAAGGAACCCTTTAGAGA
     138▶euAsnLysIleValArgMetTyrSerProThrSerIleLeuAspIleArgGlnGlyProLysGluProPheArgAs
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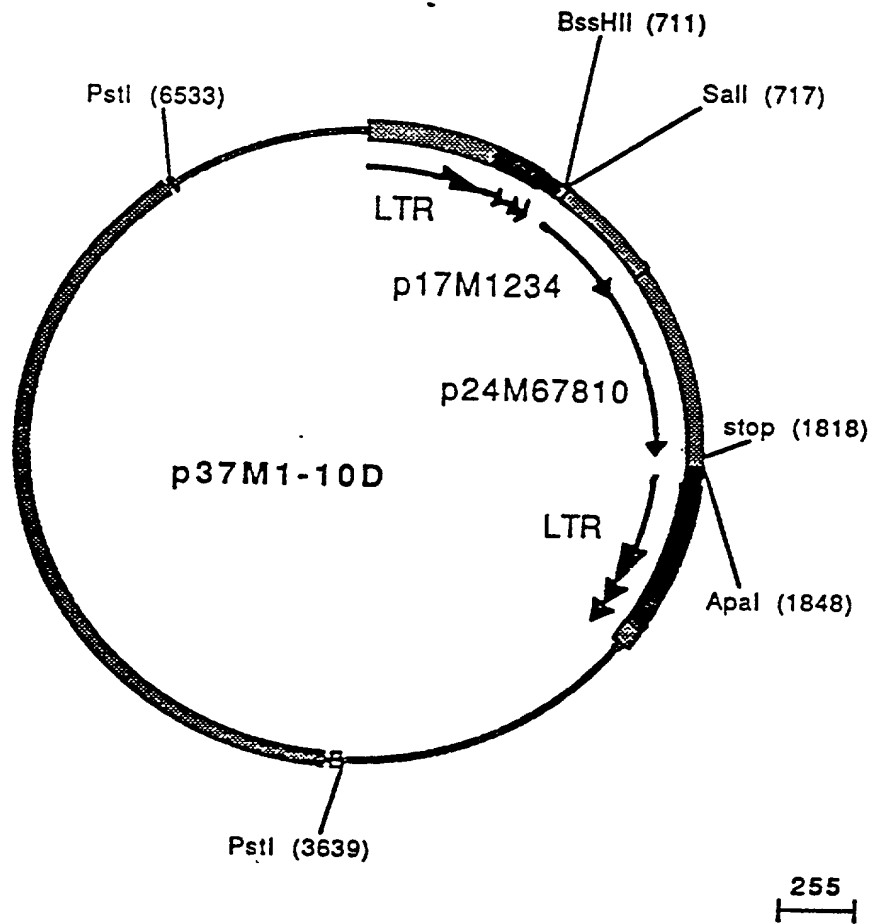
Fig. 14 B

1613 CTATGTAGACCGGTTCTATAAAACTCTAAGAGCTGAGCAAGCTTCACAGGAGGTAAAAAATTGGATGACAGAAACC
163▶ pTyrValAspArgPheTyrLysThr LeuArgAl aGl uGl nAl aSer Gl nGl uVal LysAsnTrpMet Thr Gl uThr

1689 TTGTTGGTCCAAAATGCGAACCCAGATTGTAAGACCATCCTGAAGGCTCTCGGCCCAGCGGCTACACTAGAAGAAA
189▶ LeuLeuVal Gl nAsnAl aAsnProAspCysLysThr I l eLeuLysAl aLeuGl yProAl aAl aThr LeuGl uGl uM

stop (1818)   Xbal (1838)
1765 TGATGACAGCATGTCAGGGAGTAGGAGGACCCGGCCATAAGGCAAGAGTTTGTAGGGATCCACTAGTTCTAGACT
214▶ et Met Thr Al aCysGl nGl yVal Gl yGl yProGl yHi sLysAl aArgVal Leu

Apal (1848)
1841 CGAGGGGGGG CCCGGTACCT TTAAGACCAA .TGACTTACAA GGCAGCTGTA GATCTTAGCC ACTTTTTAAA

1911 AGAAAAGGGG GGACTGGAAG GGCTAATTCA CTCCCAAAGA AGACAAGATA TCCTTGATCT GTGGATCTAC .

1981 CACACACAAG GCTACTTCCC TGATTGGCAG AACTACACAC CAGGGCCAGG GGTCAGATAT CCACTGACCT

2051 TTGGATGGTG CTACAAGCTA GTACCAGTTG AGCCAGATAA GGTAGAAGAG GCCAATAAAG GAGAGAACAC

2121 CAGCTTGTTA CACCCTGTGA GCCTGCATGG AATGGATGAC CCTGAGAGAG AAGTGTTAGA GTGGAGGTTT

2191 GACAGCCGCC TAGCATTTCA TCACGTGGCC CGAGAGCTGC ATCCGGAGTA CTTCAAGAAC TGCTGACATC

2261 GAGCTTGCTA CAAGGGACTT TCCGCTGGGG ACTTTCCAGG GAGGCGTGGC CTGGGCGGGA CTGGGGAGTG

2331 GCGAGCCCTC AGATGCTGCA TATAAGCAGC TGCTTTTTGC CTGTACTGGG TCTCTCTGGT TAGACCAGAT

2401 CTGAGCCTGG GAGCTCTCTG GCTAACTAGG GAACCCACTG CTTAAGCCTC AATAAAGCTT GCCTTGAGTG

2471 CTTCAAGTAG TGTGTGCCCG TCTGTTGTGT GACTCTGGTA ACTAGAGATC CCTCAGACCC TTTTAGTCAG

2541 TGTGGAAAAT CTCTAGCACC CCCCAGGAGG TAGAGGTTGC AGTGAGCCAA GATCGCGCCA CTGCATTCCA

2611 GCCTGGGCAA GAAAACAAGA CTGTCTAAAA TAATAATAAT AAGTTAAGGG TATTAAATAT ATTTATACAT
2681 GGAGGTCATA AAAATATATA TATTTGGGCT GGGCGCAGTG GCTCACACCT GCGCCCGGCC CTTTGGGAGG
2751 CCGAGGCAGG TGGATCACCT GAGTTTGGGA GTTCCAGACC AGCCTGACCA ACATGGAGAA ACCCCTTCTC
2821 TGTGTATTTT TAGTAGATTT TATTTTATGT GTATTTTATT CACAGGTATT TCTGGAAAAC TGAAACTGTT
2891 TTTCCTCTAC TCTGATACCA CAAGAATCAT CAGCACAGAG GAAGACTTCT GTGATCAAAT GTGGTGGGAG
2961 AGGGAGGTTT TCACCAGCAC ATGAGCAGTC AGTTCTGCCG CAGACTCGGC GGGTGTCCTT CGGTTCAGTT
3031 CCAACACCGC CTGCCTGGAG AGAGGTCAGA CCACAGGGTG AGGGCTCAGT CCCCAAGACA TAAACACCCA
3101 AGACATAAAC ACCCAACAGG TCCACCCCGC CTGCTGCCCA GGCAGAGCCG ATTCACCAAG ACGGGAATTA
3171 GGATAGAGAA AGAGTAAGTC ACACAGAGCC GGCTGTGCGG GAGAACGGAG TTCTATTATG ACTCAAATCA
3241 GTCTCCCCAA GCATTCGGGG ATCAGAGTTT TTAAGGATAA CTTAGTGTGT AGGGGGCCAG TGAGTTGGAG
3311 ATGAAAGCGT AGGGAGTCGA AGGTGTCCTT TTGCGCCGAG TCAGTTCCTG GGTGGGGGCC ACAAGATCGG
3381 ATGAGCCAGT TTATCAATCC GGGGGTGCCA GCTGATCCAT GGAGTGCAGG GTCTGCAAAA TATCTCAAGC
3451 ACTGATTGAT CTTAGGTTTT ACAATAGTGA TGTTACCCCA GGAACAATTT GGGGAAGGTC AGAATCTTGT
3521 AGCCTGTAGC TGCATGACTC CTAAACCATA ATTTCTTTTT TGTTTTTTTT TTTTTATTTT TGAGACAGGG

Pstl (3639)
3591 TCTCACTCTG TCACCTAGGC TGGAGTGCAG TGGTGCAATC ACAGCTCACT GCAGCCCCTA GAGCGGCCGC
3661 CACCGCGGTG GAGCTCCAAT TCGCCCTATA GTGAGTCGTA TTACAATTCA CTGGCCGTCG TTTTACAACG
3731 TCGTGACTGG GAAAACCCTG GCGTTACCCA ACTTAATCGC CTTGCAGCAC ATCCCCCTTT CGCCAGCTGG
3801 CGTAATAGCG AAGAGGCCCG CACCGATCGC CCTTCCCAAC AGTTGCGCAG CCTGAATGGC GAATGGCGCG
3871 AAATTGTAAA CGTTAATATT TTGTTAAAAT TCGCGTTAAA TTTTTGTTAA ATCAGCTCAT TTTTTAACCA
3941 ATAGGCCGAA ATCGGCAAAA TCCCTTATAA ATCAAAAGAA TAGACCGAGA TAGGGTTGAG TGTTGTTCCA
4011 GTTTGGAACA AGAGTCCACT ATTAAAGAAC GTGGACTCCA ACGTCAAAGG GCGAAAAACC GTCTATCAGG
4081 GCGATGGCCC ACTACGTGAA CCATCACCCT AATCAAGTTT TTTGGGGTCG AGGTGCCGTA AAGCACTAAA
4151 TCGGAACCCT AAAGGGAGCC CCCGATTTAG AGCTTGACGG GGAAAGCCGG CGAACGTGGC GAGAAAGGAA
4221 GGGAAGAAAG CGAAAGGAGC GGGCGCTAGG GCGCTGGCAA GTGTAGCGGT CACGCTGCGC GTAACCACCA
4291 CACCCGCCGC GCTTAATGCG CCGCTACAGG GCGCGTCCCA GGTGGCACTT TCGGGGAAA TGTGCGCGGA
4361 ACCCCTATTT GTTTATTTTT CTAAATACAT TCAAATATGT ATCCGCTCAT GAGACAATAA CCCTGATAAA

Fig. 14 C

```
4431  TGCTTCAATA ATATTGAAAA AGGAAGAGTA TGAGTATTCA ACATTTCCGT GTCGCCCTTA TTCCCTTTTT
4501  TGCGGCATTT TGCCTTCCTG TTTTTGCTCA CCCAGAAACG CTGGTGAAAG TAAAAGATGC TGAAGATCAG
4571  TTGGGTGCAC GAGTGGGTTA CATCGAACTG GATCTCAACA GCGGTAAGAT CCTTGAGAGT TTTCGCCCCG
4641  AAGAACGTTT TCCAATGATG AGCACTTTTA AAGTTCTGCT ATGTGGCGCG GTATTATCCC GTATTGACGC
4711  CGGGCAAGAG CAACTCGGTC GCCGCATACA CTATTCTCAG AATGACTTGG TTGAGTACTC ACCAGTCACA
4781  GAAAAGCATC TTACGGATGG CATGACAGTA AGAGAATTAT GCAGTGCTGC CATAACCATG AGTGATAACA
4851  CTGCGGCCAA CTTACTTCTG ACAACGATCG GAGGACCGAA GGAGCTAACC GCTTTTTTGC ACAACATGGG
4921  GGATCATGTA ACTCGCCTTG ATCGTTGGGA ACCGGAGCTG AATGAAGCCA TACCAAACGA CGAGCGTGAC
4991  ACCACGATGC CTGTAGCAAT GGCAACAACG TTGCGCAAAC TATTAACTGG CGAACTACTT ACTCTAGCTT
5061  CCCGGCAACA ATTAATAGAC TGGATGGAGG CGGATAAAGT TGCAGGACCA CTTCTGCGCT CGGCCCTTCC
5131  GGCTGGCTGG TTTATTGCTG ATAAATCTGG AGCCGGTGAG CGTGGGTCTC GCGGTATCAT TGCAGCACTG
5201  GGGCCAGATG GTAAGCCCTC CCGTATCGTA GTTATCTACA CGACGGGGAG TCAGGCAACT ATGGATGAAC
5271  GAAATAGACA GATCGCTGAG ATAGGTGCCT CACTGATTAA GCATTGGTAA CTGTCAGACC AAGTTTACTC
5341  ATATATACTT TAGATTGATT TAAAACTTCA TTTTTAATTT AAAAGGATCT AGGTGAAGAT CCTTTTTGAT
5411  AATCTCATGA CCAAAATCCC TTAACGTGAG TTTTCGTTCC ACTGAGCGTC AGACCCCGTA GAAAAGATCA
5481  AAGGATCTTC TTGAGATCCT TTTTTTCTGC GCGTAATCTG CTGCTTGCAA ACAAAAAAAC CACCGCTACC
5551  AGCGGTGGTT TGTTTGCCGG ATCAAGAGCT ACCAACTCTT TTTCCGAAGG TAACTGGCTT CAGCAGAGCG
5621  CAGATACCAA ATACTGTCCT TCTAGTGTAG CCGTAGTTAG GCCACCACTT CAAGAACTCT GTAGCACCGC
5691  CTACATACCT CGCTCTGCTA ATCCTGTTAC CAGTGGCTGC TGCCAGTGGC GATAAGTCGT GTCTTACCGG
5761  GTTGGACTCA AGACGATAGT TACCGGATAA GGCGCAGCGG TCGGGCTGAA CGGGGGGTTC GTGCACACAG
5831  CCCAGCTTGG AGCGAACGAC CTACACCGAA CTGAGATACC TACAGCGTGA GCTATGAGAA AGCGCCACGC
5901  TTCCCGAAGG GAGAAAGGCG GACAGGTATC CGGTAAGCGG CAGGGTCGGA ACAGGAGAGC GCACGAGGGA
5971  GCTTCCAGGG GGAAACGCCT GGTATCTTTA TAGTCCTGTC GGGTTTCGCC ACCTCTGACT TGAGCGTCGA
6041  TTTTTGTGAT GCTCGTCAGG GGGGCGGAGC CTATGGAAAA ACGCCAGCAA CGCGGCCTTT TTACGGTTCC
6111  TGGCCTTTTG CTGGCCTTTT GCTCACATGT TCTTTCCTGC GTTATCCCCT GATTCTGTGG ATAACCGTAT
6181  TACCGCCTTT GAGTGAGCTG ATACCGCTCG CCGCAGCCGA ACGACCGAGC GCAGCGAGTC AGTGAGCGAG
6251  GAAGCGGAAG AGCGCCCAAT ACGCAAACCG CCTCTCCCCG CGCGTTGGCC GATTCATTAA TGCAGCTGGC
6321  ACGACAGGTT TCCCGACTGG AAAGCGGGCA GTGAGCGCAA CGCAATTAAT GTGAGTTAGC TCACTCATTA
6391  GGCACCCCAG GCTTTACACT TTATGCTTCC GGCTCGTATG TTGTGTGGAA TTGTGAGCGG ATAACAATTT
6461  CACACAGGAA ACAGCTATGA CCATGATTAC GCCAAGCTCG GAATTAACCC TCACTAAAGG GAACAAAAGC
            PstI (6533)
6531  TGCTGCAGGG TCCCTAACTG CCAAGCCCCA CAGTGTGCCC TGAGGCTGCC CCTTCCTTCT AGCGGCTGCC
6601  CCCACTCGGC TTTGCTTTCC CTAGTTTCAG TTACTTGCGT TCAGCCAAGG TCTGAAACTA GGTGCGCACA
6671  GAGCGGTAAG ACTGCGAGAG AAAGAGACCA GCTTTACAGG GGGTTTATCA CAGTGCACCC TGACAGTCGT
6741  CAGCCTCACA GGGGGGTTTAT CACATTGCAC CCTGACAGTC GTCAGCCTCA CAGGGGGTTT ATCACAGTGC
6811  ACCCTTACAA TCATTCCATT TGATTCACAA TTTTTTTAGT CTCTACTGTG CCTAACTTGT AAGTTAAATT
6881  TGATCAGAGG TGTGTTCCCA GAGGGGAAAA CAGTATATAC AGGGTTCAGT ACTATCGCAT TTCAGGCCTC
6951  CACCTGGGTC TTGGAATGTG TCCCCCGAGG GGTGATGACT ACCTCAGTTG GATCTCCACA GGTCACAGTG
7021  ACACAAGATA ACCAAGACAC CTCCCAAGGC TACCACAATG GGCCGCCCTC CACGTGCACA TGGCCGGAGG
7091  AACTGCCATG TCGGAGGTGC AAGCACACCT GCGCATCAGA GTCCTTGGTG TGGAGGGAGG GACCAGCGCA
7161  GCTTCCAGCC ATCCACCTGA TGAACAGAAC CTAGGGAAAG CCCCAGTTCT ACTTACACCA GGAAAGGC
```

Fig. 14   D